

SEQUENCE LISTING

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<110> Cortes, J
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<120> BIOSYNTHESIS GENES & TRANSFER OF 6-DESOXYHEXOSES IN
SACCHAROPOLYSPORA ERYTHRAEA AND IN STREPTOMYCES
ANTIBIOTICUS AND THEIR USE

<130> 146.1335

<140> 09/463705

<141> 2000-02-23

<150> PCT/FR98/01593

<151> 1998-07-21

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<151> 1988-06-12

<150> 97/09458

<151> 1997-07-25

<160> 61

<170> PatentIn Ver. 2.1

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<213> Saccharopolyspora erythraea

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<213> Saccharopolyspora erythraea

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ctc acc gac ggc atc gac cgg acg gtg gcc gcc ctg acc ccc acc gag Leu Thr Asp Gly Ile Asp Arg Thr Val Ala Ala Leu Thr Pro Thr Glu 305 310 315 320			1201
gag cac ta gtg cgg gta ctg ctg acg tcc ttc gcg cac cgc acg cac Glu His Met Arg Val Leu Leu Thr Ser Phe Ala His Arg Thr His 325 330 335			1248
ttc cag gga ctg gtc ccg ctg gcg tgg gcg ctg cgc acc gcg ggt cac Phe Gln Gly Leu Val Pro Leu Ala Trp Ala Leu Arg Thr Ala Gly His 340 345 350			1296
gac gtg cgc gtg gcc gcc cag ccc gcg ctc acc gac gcg gtc atc ggc Asp Val Arg Val Ala Ala Gln Pro Ala Leu Thr Asp Ala Val Ile Gly 355 360 365			1344
gcc ggt ctc acc gcg gta ccc gtc ggc tcc gac cac cgg ctg ttc gac Ala Gly Leu Thr Ala Val Pro Val Gly Ser Asp His Arg Leu Phe Asp 370 375 380			1392
atc gtc ccg gaa gtc gcc gct cag gtg cac cgc tac tcc ttc tac ctg Ile Val Pro Glu Val Ala Ala Gln Val His Arg Tyr Ser Phe Tyr Leu 385 390 395			1440
gac ttc tac cac cgc gag cag gag ctg cac tcg tgg gag ttc ctg ctc Asp Phe Tyr His Arg Glu Gln Glu Leu His Ser Trp Glu Phe Leu Leu 400 405 410 415			1488
ggc atg cag gag gcc acc tcg cgg tgg gta tac ccg gtg gtc aac aac Gly Met Gln Glu Ala Thr Ser Arg Trp Val Tyr Pro Val Val Asn Asn			1536

420										425					430					
gac	tcc	ttc	gtc	gcc	gag	ctg	gtc	gac	ttc	gcc	cgg	gac	tgg	cgt	cct	1584				
Asp	Ser	Phe	Val	Ala	Glu	Leu	Val	Asp	Phe	Ala	Arg	Asp	Trp	Arg	Pro					
435				440				445												
gac	ctg	gtg	ctc	tgg	gag	cgg	ttc	acc	ttc	gcc	ggc	gcc	gtc	gcg	gcc	1632				
Asp	Leu	Val	Leu	Trp	Glu	Pro	Phe	Thr	Phe	Ala	Gly	Ala	Val	Ala	Ala					
450				455				460												
cgg	gcc	tgc	gga	gcc	gcg	cac	gcc	cgg	ctg	ctg	tgg	ggc	agc	gac	ctc	1680				
Arg	Ala	Cys	Gly	Ala	Ala	His	Ala	Arg	Leu	Leu	Trp	Gly	Ser	Asp	Leu					
465				470				475												
acc	ggc	tac	ttc	cgc	ggc	cgg	ttc	cag	gcg	caa	cgc	ctg	cga	cgg	ccg	1728				
Thr	Gly	Tyr	Phe	Arg	Gly	Arg	Phe	Gln	Ala	Gln	Arg	Leu	Arg	Arg	Pro					
480				485				490				495								
ccg	gag	gac	cgg	ccg	gac	ccg	ctg	ggc	acg	tgg	ctg	acc	gag	gtc	gcg	1776				
Pro	Glu	Asp	Arg	Pro	Asp	Pro	Leu	Gly	Thr	Trp	Leu	Thr	Glu	Val	Ala					
500				505				510												
ggg	cgc	ttc	ggc	gtc	gaa	ttc	ggc	gag	gac	ctc	gcg	gtc	ggg	cag	tgg	1824				
Gly	Arg	Phe	Gly	Val	Glu	Phe	Gly	Glu	Asp	Leu	Ala	Val	Gly	Gln	Trp					
515				520				525												
tcg	gtc	gac	cag	ttg	ccg	ccg	agt	ttc	cgg	ctg	gac	acc	gga	atg	gaa	1872				
Ser	Val	Asp	Gln	Leu	Pro	Pro	Ser	Phe	Arg	Leu	Asp	Thr	Gly	Met	Glu					
530				535				540												
acc	gtt	gtc	gcg	cgg	acc	ctg	ccc	tac	aac	ggc	gcg	tcg	gtg	gtt	ccg	1920				
Thr	Val	Val	Ala	Arg	Thr	Leu	Pro	Tyr	Asn	Gly	Ala	Ser	Val	Val	Pro					
545				550				555												
gac	tgg	ctc	aag	aag	ggc	agt	gcg	act	cga	cgc	atc	tgc	att	acc	gga	1968				
Asp	Trp	Leu	Lys	Lys	Gly	Ser	Ala	Thr	Arg	Arg	Ile	Cys	Ile	Thr	Gly					
560				565				570				575								
ggg	ttc	tcc	gga	ctc	ggg	ctc	gcc	gcc	gat	gcc	gat	cag	ttc	gcg	cgg	2016				
Gly	Phe	Ser	Gly	Leu	Gly	Leu	Ala	Ala	Asp	Ala	Asp	Gln	Phe	Ala	Arg					
580				585				590												
acg	ctc	gcg	cag	ctc	gcg	cga	ttc	gat	ggc	gaa	atc	gtg	gtt	acg	ggg	2064				
Thr	Leu	Ala	Gln	Leu	Ala	Arg	Phe	Asp	Gly	Glu	Ile	Val	Val	Thr	Gly					
595				600				605												
tcc	ggg	ccg	gat	acc	tcc	gcg	gta	ccg	gac	aac	att	cgt	ttg	gtg	gat	2112				
Ser	Gly	Pro	Asp	Thr	Ser	Ala	Val	Pro	Asp	Asn	Ile	Arg	Leu	Val	Asp					
610				615				620												
ttc	gtt	ccg	atg	ggc	gtt	ctg	ctc	cag	aac	tgc	gcg	gcg	atc	atc	cac	2160				
Phe	Val	Pro	Met	Gly	Val	Leu	Leu	Gln	Asn	Cys	Ala	Ala	Ile	Ile	His					
625				630				635												
cac	ggc	ggg	gcc	gga	acc	tgg	gcc	acg	gca	ctg	cac	cac	gga	att	ccg	2208				
His	Gly	Gly	Ala	Gly	Thr	Trp	Ala	Thr	Ala	Leu	His	His	Gly	Ile	Pro					
640				645				650				655								

caa ata tca gtt gca cat gaa tgg gat tgc atg cta cgc ggc cag cag	2256
Gln Ile Ser Val Ala His Glu Trp Asp Cys Met Leu Arg Gly Gln Gln	
660 665 670	
acc gcg gaa ctg ggc gcg gga atc tac ctc cgg ccg gac gag gtc gat	2304
Thr Ala Glu Leu Gly Ala Gly Ile Tyr Leu Arg Pro Asp Glu Val Asp	
675 680 685	
gcc gac tca ttg gcg agc gcc ctc acc cag gtg gtc gag gac ccc acc	2352
Ala Asp Ser Leu Ala Ser Ala Leu Thr Gln Val Val Glu Asp Pro Thr	
690 695 700	
tac acc gag aac gcg gtg aag ctt cgc gag gag gcg ctg tcc gac ccg	2400
Tyr Thr Glu Asn Ala Val Lys Leu Arg Glu Glu Ala Leu Ser Asp Pro	
705 710 715	
acg ccg cag gag atc gtc ccg cga ctg gag gaa ctc acg cgc cgc cac	2448
Thr Pro Gln Glu Ile Val Pro Arg Leu Glu Glu Leu Thr Arg Arg His	
720 725 730 735	
gcc ggc tagcgggtttc cgaccgacaa gtccgtccga cagcacacct ccggagggag	2504
Ala Gly	
caggg atg tac gag ggc ggg ttc gcc gag ctt tac gac cgg ttc tac cgc	2554
Met Tyr Glu Gly Gly Phe Ala Glu Leu Tyr Asp Arg Phe Tyr Arg	
740 745 750	
ggc ccg ggc aag gac tac gcg gcc gag gcc gcg cag gtc gcg ccg ctg	2602
Gly Arg Gly Lys Asp Tyr Ala Ala Glu Ala Ala Gln Val Ala Arg Leu	
755 760 765	
gtc aga gac cgc ctg ccc tcg gct tcc tcg ctg ctc gac gtg gcc tgc	2650
Val Arg Asp Arg Leu Pro Ser Ala Ser Ser Leu Leu Asp Val Ala Cys	
770 775 780	
ggg acc ggc acc cac ctg cgc ccg ttc gcc gac ctc ttc gac gac gtg	2698
Gly Thr Gly Thr His Leu Arg Arg Phe Ala Asp Leu Phe Asp Asp Val	
785 790 795 800	
acc ggg ctg gag ctg tcg gcg gcg atg atc gag gtc gcc ccg ccg cag	2746
Thr Gly Leu Glu Leu Ser Ala Ala Met Ile Glu Val Ala Arg Pro Gln	
805 810 815	
ctc ggc ggc atc ccg gtg ctg cag ggc gac atg cgc gac ttc gcg ctg	2794
Leu Gly Gly Ile Pro Val Leu Gln Gly Asp Met Arg Asp Phe Ala Leu	
820 825 830	
gat cgc gag ttc gac gcc gtc acc tgc atg ttc agc tcc atc ggg cac	2842
Asp Arg Glu Phe Asp Ala Val Thr Cys Met Phe Ser Ser Ile Gly His	
835 840 845	
atg cgc gac ggc gcc gag ctg gac cag gcg ctg gcg tcc ttc gcc cgc	2890
Met Arg Asp Gly Ala Glu Leu Asp Gln Ala Leu Ala Ser Phe Ala Arg	
850 855 860	
cac ctc gcc ccc ggc ggc gtc gtg gtg gtc gaa ccg tgg tgg ttc ccg	2938

His	Leu	Ala	Pro	Gly	Gly	Val	Val	Val	Val	Glu	Pro	Trp	Trp	Phe	Pro		
865					870					875					880		
gag	gac	ttc	ctc	gac	ggc	tac	gtg	gcc	ggg	gac	gtg	gtg	cgc	gac	ggc	2986	
Glu	Asp	Phe	Leu	Asp	Gly	Tyr	Val	Ala	Gly	Asp	Val	Val	Arg	Asp	Gly		
				885					890					895			
gac	ctg	acg	atc	tcg	cgc	gtc	tcg	cac	tcc	gtg	cgc	gcc	ggc	ggc	gcg	3034	
Asp	Leu	Thr	Ile	Ser	Arg	Val	Ser	His	Ser	Val	Arg	Ala	Gly	Gly	Ala		
			900					905					910				
acc	cgg	atg	gag	atc	cac	tgg	gtc	gtg	gcc	gac	gcg	gtg	aac	ggg	ccg	3082	
Thr	Arg	Met	Glu	Ile	His	Trp	Val	Val	Ala	Asp	Ala	Val	Asn	Gly	Pro		
		915					920					925					
cgg	cac	cac	gtg	gag	cac	tac	gag	atc	acg	ctc	ttc	gag	cgg	cag	cag	3130	
Arg	His	His	Val	Glu	His	Tyr	Glu	Ile	Thr	Leu	Phe	Glu	Arg	Gln	Gln		
	930					935					940						
tac	gag	aag	gcc	ttc	acc	gcg	gcc	ggg	tgc	gct	gtg	cag	tac	ctg	gag	3178	
Tyr	Glu	Lys	Ala	Phe	Thr	Ala	Ala	Gly	Cys	Ala	Val	Gln	Tyr	Leu	Glu		
945					950				955						960		
ggc	gga	ccc	tcc	gga	cgc	ggg	ttg	ttc	gtc	ggg	gtg	cgc	gga			3220	
Gly	Gly	Pro	Ser	Gly	Arg	Gly	Leu	Phe	Val	Gly	Val	Arg	Gly				
				965					970								
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cccgccgtga	ccggaccctt	acagtga	gtg	cgg	gtc	ttg	atc	gac	aac	gcc	cgg					3334	
			Met	Arg	Val	Leu	Ile	Asp	Asn	Ala	Arg						
					975					980							
cgg	cag	caa	gcg	gag	ccg	tcg	acg	aca	ccg	cag	gga	gag	tcg	atg	ggg	3382	
Arg	Gln	Gln	Ala	Glu	Pro	Ser	Thr	Thr	Pro	Gln	Gly	Glu	Ser	Met	Gly		
	985					990					995						
gat	cgg	acc	ggc	gac	cgg	acg	att	ccg	gaa	tcc	tcg	cag	acc	gca	acg	3430	
Asp	Arg	Thr	Gly	Asp	Arg	Thr	Ile	Pro	Glu	Ser	Ser	Gln	Thr	Ala	Thr		
1000					1005				1010					1015			
cgt	ttc	ctg	ctc	ggc	gac	ggc	gga	atc	ccc	acc	gcc	acg	gcg	gaa	acc	3478	
Arg	Phe	Leu	Leu	Gly	Asp	Gly	Gly	Ile	Pro	Thr	Ala	Thr	Ala	Glu	Thr		
				1020					1025					1030			
cac	gac	tgg	ctg	acc	cgc	aac	ggc	gcc	gag	cag	cgg	ctc	gag	gtg	gcg	3526	
His	Asp	Trp	Leu	Thr	Arg	Asn	Gly	Ala	Glu	Gln	Arg	Leu	Glu	Val	Ala		
			1035					1040					1045				
cgc	gtg	ccg	ttc	agc	gcc	atg	gac	cgc	tgg	tcg	ttc	cag	ccc	gag	gac	3574	
Arg	Val	Pro	Phe	Ser	Ala	Met	Asp	Arg	Trp	Ser	Phe	Gln	Pro	Glu	Asp		
		1050					1055					1060					
ggc	agg	ctc	gcc	cac	gag	tcc	ggg	cgc	ttc	ttc	tcc	atc	gag	ggc	ctg	3622	
Gly	Arg	Leu	Ala	His	Glu	Ser	Gly	Arg	Phe	Phe	Ser	Ile	Glu	Gly	Leu		
	1065					1070					1075						

cac gtg cgg acg aac ttc ggc tgg cgg cgg gac tgg atc cag ccc atc	3670
His Val Arg Thr Asn Phe Gly Trp Arg Arg Asp Trp Ile Gln Pro Ile	
1080 1085 1090 1095	
atc gtg cag ccc gag atc ggc ttc ctc ggc ctc atc gtc aag gag ttc	3718
Ile Val Gln Pro Glu Ile Gly Phe Leu Gly Leu Ile Val Lys Glu Phe	
1100 1105 1110	
gac ggt gtg ctg cac gtg ctg gcg cag gcc aag gcc gag ccg ggc aac	3766
Asp Gly Val Leu His Val Leu Ala Gln Ala Lys Ala Glu Pro Gly Asn	
1115 1120 1125	
atc aac gcc gtc cag ctc tcc ccg acc ctg cag gcg acc cgc agc aac	3814
Ile Asn Ala Val Gln Leu Ser Pro Thr Leu Gln Ala Thr Arg Ser Asn	
1130 1135 1140	
tac acc ggc gtc cac cgc ggc tcg aag gtc cgg ttc atc gag tac ttc	3862
Tyr Thr Gly Val His Arg Gly Ser Lys Val Arg Phe Ile Glu Tyr Phe	
1145 1150 1155	
aac ggc acg cgc ccg agc cgg atc ctc gtc gac gtg ctc cag tcc gag	3910
Asn Gly Thr Arg Pro Ser Arg Ile Leu Val Asp Val Leu Gln Ser Glu	
1160 1165 1170 1175	
cag ggc gcg tgg ttc ctg cgc aag cgc aac cgg aac atg gtc gtc gag	3958
Gln Gly Ala Trp Phe Leu Arg Lys Arg Asn Arg Asn Met Val Val Glu	
1180 1185 1190	
gtg ttc gac gac ctg ccc gag cac ccg aac ttc cgg tgg ctg acc gtc	4006
Val Phe Asp Asp Leu Pro Glu His Pro Asn Phe Arg Trp Leu Thr Val	
1195 1200 1205	
gcg cag ctg cgg gcg atg ctg cac cac gac aac gtg gtg aac atg gac	4054
Ala Gln Leu Arg Ala Met Leu His His Asp Asn Val Val Asn Met Asp	
1210 1215 1220	
ctg cgc acc gtg ctg gcc tgc gtc ccg acc gcc gtg gag cgg gac cgg	4102
Leu Arg Thr Val Leu Ala Cys Val Pro Thr Ala Val Glu Arg Asp Arg	
1225 1230 1235	
gcc gac gac gtg ctc gcg cgc ctg ccc gag ggc tcg ttc cag gcc cgg	4150
Ala Asp Asp Val Leu Ala Arg Leu Pro Glu Gly Ser Phe Gln Ala Arg	
1240 1245 1250 1255	
ctg ctg cac tcg ttc atc ggc gcg ggc acc ccg gcc aac aac atg aac	4198
Leu Leu His Ser Phe Ile Gly Ala Gly Thr Pro Ala Asn Asn Met Asn	
1260 1265 1270	
agc ctg ctg agc tgg atc tcc gac gtg cgc gcc agg cgc gag ttc gtg	4246
Ser Leu Leu Ser Trp Ile Ser Asp Val Arg Ala Arg Arg Glu Phe Val	
1275 1280 1285	
cag cgc ggc cgc ccg ctg ccc gac atc gag cgc agc ggg tgg atc cgc	4294
Gln Arg Gly Arg Pro Leu Pro Asp Ile Glu Arg Ser Gly Trp Ile Arg	
1290 1295 1300	
cgc gac gac ggc atc gag cac gag gag aag aag tac ttc gac gtc ttc	4342

Arg Asp Asp Gly Ile Glu His Glu Glu Lys Lys Tyr Phe Asp Val Phe
 1305 1310 1315
 ggc gtc acg gtg gcg acc agc gac cgc gag gtc aac tcg tgg atg cag 4390
 Gly Val Thr Val Ala Thr Ser Asp Arg Glu Val Asn Ser Trp Met Gln
 1320 1325 1330 1335
 ccg ctg ctc tcg ccc gcc aac aac ggc ctg ctc gcc ctg ctg gtc aag 4438
 Pro Leu Leu Ser Pro Ala Asn Asn Gly Leu Leu Ala Leu Leu Val Lys
 1340 1345 1350
 gac atc ggc ggc acg ttg cac gcg ctc gtg cag ctg cgc acc gag gcg 4486
 Asp Ile Gly Gly Thr Leu His Ala Leu Val Gln Leu Arg Thr Glu Ala
 1355 1360 1365
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 Gly Gly Met Asp Val Ala Glu Leu Ala Pro Thr Val His Cys Gln Pro
 1370 1375 1380
 gac aac tac gcc gac gcg ccc gag gag ttc cga ccg gcc tat gtg gac 4582
 Asp Asn Tyr Ala Asp Ala Pro Glu Glu Phe Arg Pro Ala Tyr Val Asp
 1385 1390 1395
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 Tyr Val Leu Asn Val Pro Arg Ser Gln Val Arg Tyr Asp Ala Trp His
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 tcc gag gag ggc ggc cgg ttc tac cgc aac gag aac cgg tac atg ctg 4678
 Ser Glu Glu Gly Gly Arg Phe Tyr Arg Asn Glu Asn Arg Tyr Met Leu
 1420 1425 1430
 atc gag gtg ccc gcc gac ttc gac gcc agt gcc gct ccc gac cac cgg 4726
 Ile Glu Val Pro Ala Asp Phe Asp Ala Ser Ala Ala Pro Asp His Arg
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 tgg atg acc ttc gac cag atc acc tac ctg ctc ggg cac agc cac tac 4774
 Trp Met Thr Phe Asp Gln Ile Thr Tyr Leu Leu Gly His Ser His Tyr
 1450 1455 1460
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 Val Asn Ile Gln Leu Arg Ser Ile Ile Ala Cys Ala Ser Ala Val Tyr
 1465 1470 1475
 acc agg acc gcc gga tgaaacgcgc gctgaccgac ctggcgatct tcggcgggccc 4877
 Thr Arg Thr Ala Gly
 1480
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 cg atg aac aca act cgt acg gca acc gcc cag gaa gcg ggg gtc gcc 6124
 Met Asn Thr Thr Arg Thr Ala Thr Ala Gln Glu Ala Gly Val Ala
 1485 1490 1495
 gac gcg gcg cgc ccg gac gtc gac cgg cgg gcg gtc gtg cgg gcg ctg 6172
 Asp Ala Ala Arg Pro Asp Val Asp Arg Arg Ala Val Val Arg Ala Leu
 1500 1505 1510 1515
 agc tcg gag gtc tcc cgc gtc acc ggc gcc ggt gac ggt gac gcc gac 6220
 Ser Ser Glu Val Ser Arg Val Thr Gly Ala Gly Asp Gly Asp Ala Asp
 1520 1525 1530
 gtg cag gcc gcc cgg ctc gcc gac ctc gcc gcg cac tac ggg gcg cac 6268
 Val Gln Ala Ala Arg Leu Ala Asp Leu Ala Ala His Tyr Gly Ala His
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 Pro Phe Thr Pro Leu Glu Gln Thr Arg Ala Arg Leu Gly Leu Asp Arg
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 Ala Glu Phe Ala His Leu Leu Asp Leu Phe Gly Arg Ile Pro Asp Leu
 1565 1570 1575
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 Gly Thr Ala Val Glu His Gly Pro Ala Gly Lys Tyr Trp Ser Asn Thr
 1580 1585 1590 1595

atc aag ccg ctg gac gcc gca ggc gca ctg gac gcg gcg gtc tac cgc Ile Lys Pro Leu Asp Ala Ala Gly Ala Leu Asp Ala Ala Val Tyr Arg 1600 1605 1610	6460
aag cct gcc ttc ccc tac agc gtc ggc ctg tac ccc ggg ccg acg tgc Lys Pro Ala Phe Pro Tyr Ser Val Gly Leu Tyr Pro Gly Pro Thr Cys 1615 1620 1625	6508
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gcc gca tcg gtc ccg gcg ggc aac gag acg ctg gcc gcg atc atc gac Ala Ala Ser Val Pro Ala Gly Asn Glu Thr Leu Ala Ala Ile Ile Asp 1645 1650 1655	6604
gag gtg ccc acg gac aac ccg aag gcg atg tac atg tcg ggc ggg ctc Glu Val Pro Thr Asp Asn Pro Lys Ala Met Tyr Met Ser Gly Gly Leu 1660 1665 1670 1675	6652
gag ccg ctg acc aac ccc ggt ctc ggc gag ctg gtg tcg cac gcc gcc Glu Pro Leu Thr Asn Pro Gly Leu Gly Glu Leu Val Ser His Ala Ala 1680 1685 1690	6700
ggg cgc ggt ttc gac ctc acc gtc tac acc aac gcc ttc gcc ctc acc Gly Arg Gly Phe Asp Leu Thr Val Tyr Thr Asn Ala Phe Ala Leu Thr 1695 1700 1705	6748
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ctg cgg atg cgc gcc gag cgg gac gcg ccg atc cgg ctc ggc ttc aac Leu Arg Met Arg Ala Glu Arg Asp Ala Pro Ile Arg Leu Gly Phe Asn 1760 1765 1770	6940
cac atc atc ctg ccg gga cgg gcc gac cgg ctc acc gac ctc gtc gac His Ile Ile Leu Pro Gly Arg Ala Asp Arg Leu Thr Asp Leu Val Asp 1775 1780 1785	6988
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gtg acg gtg cgc gag gac tac agc ggc cgc gac gac ggc cgg ctg tcg Val Thr Val Arg Glu Asp Tyr Ser Gly Arg Asp Asp Gly Arg Leu Ser 1805 1810 1815	7084

gac tcc gag cgc aac gag ctg cgc gag ggc ctg gtg cgg ttc gtc gac Asp Ser Glu Arg Asn Glu Leu Arg Glu Gly Leu Val Arg Phe Val Asp 1820 1825 1830 1835	7132
tac gcc gcc gag cgg acc ccg ggc atg cac atc gac ctg ggc tac gcc Tyr Ala Ala Glu Arg Thr Pro Gly Met His Ile Asp Leu Gly Tyr Ala 1840 1845 1850	7180
ctg gag agc ctg cgg cgg ggt gtg gac gcc gag ctg ctg cgc atc cgg Leu Glu Ser Leu Arg Arg Gly Val Asp Ala Glu Leu Leu Arg Ile Arg 1855 1860 1865	7228
ccg gag acg atg cgt ccc acc gcg cac ccc cag gtc gcg gtg cag atc Pro Glu Thr Met Arg Pro Thr Ala His Pro Gln Val Ala Val Gln Ile 1870 1875 1880	7276
gac ctg ctc ggc gac gtc tac ctc tac cgc gag gcg ggc ttc ccg gag Asp Leu Leu Gly Asp Val Tyr Leu Tyr Arg Glu Ala Gly Phe Pro Glu 1885 1890 1895	7324
ctg gag ggc gcc acc cgc tac atc gcg ggc cgg gtc acc ccg tcg acc Leu Glu Gly Ala Thr Arg Tyr Ile Ala Gly Arg Val Thr Pro Ser Thr 1900 1905 1910 1915	7372
agc ctg cgc gag gtg gtg gag aac ttc gtg ctg gag aac gag ggc gtg Ser Leu Arg Glu Val Val Glu Asn Phe Val Leu Glu Asn Glu Gly Val 1920 1925 1930	7420
cag ccc cgc ccc ggc gac gag tac ttc ctc gac ggc ttc gac cag tcg Gln Pro Arg Pro Gly Asp Glu Tyr Phe Leu Asp Gly Phe Asp Gln Ser 1935 1940 1945	7468
gtg acc gca cgg ctc aac cag ctc gaa cga gac atc gcc gac ggg tgg Val Thr Ala Arg Leu Asn Gln Leu Glu Arg Asp Ile Ala Asp Gly Trp 1950 1955 1960	7516
gag gac cac cgc ggc ttc ctg cgc gga agg tgaaccggag ttgctgagtac Glu Asp His Arg Gly Phe Leu Arg Gly Arg 1965 1970	7566
gtgagctggc g gtg gcg ggc ggt ttc gag ttc acc ccc gac ccg aag cag Met Ala Gly Gly Phe Glu Phe Thr Pro Asp Pro Lys Gln 1975 1980 1985	7616
gac cgg cgg ggc ctg ttc gtg tct ccg ctg cag gac gag gcg ttc gtg Asp Arg Arg Gly Leu Phe Val Ser Pro Leu Gln Asp Glu Ala Phe Val 1990 1995 2000	7664
ggc gcg gtg ggc cat cgg ttc ccc gtc gcc cag atg aac cac atc gtc Gly Ala Val Gly His Arg Phe Pro Val Ala Gln Met Asn His Ile Val 2005 2010 2015	7712
tcc gcc cgg ggc gtg ctg cgc ggg ctg cac ttc acc acc acc ccg ccg Ser Ala Arg Gly Val Leu Arg Gly Leu His Phe Thr Thr Thr Pro Pro 2020 2025 2030	7760
ggg cag tgc aag tac gtc tac tgc gcg cgc ggc cgg gcg ctc gac gtc	7808

Gly Gln Cys Lys Tyr Val Tyr Cys Ala Arg Gly Arg Ala Leu Asp Val
 2035 2040 2045 2050

atc gtc gac atc cgg gtc ggc tgc ccg acg ttc ggg aag tgg gac gcg 7856
 Ile Val Asp Ile Arg Val Gly Ser Pro Thr Phe Gly Lys Trp Asp Ala
 2055 2060 2065

gtg gag atg gac acc gag cac ttc cgg gcg gtc tac ttc ccc agg ggc 7904
 Val Glu Met Asp Thr Glu His Phe Arg Ala Val Tyr Phe Pro Arg Gly
 2070 2075 2080

acc gcg cac gcc ttc ctc gcg ctt gag gac gac acc ctg atg tgc tac 7952
 Thr Ala His Ala Phe Leu Ala Leu Glu Asp Asp Thr Leu Met Ser Tyr
 2085 2090 2095

ctg gtc agc acg ccg tac gtg gcc gag tac gag cag gcg atc gac ccg 8000
 Leu Val Ser Thr Pro Tyr Val Ala Glu Tyr Glu Gln Ala Ile Asp Pro
 2100 2105 2110

ttc gac ccc gcg ctg ggt ctg ccg tgg ccc gcg gac ctg gag gtc gtg 8048
 Phe Asp Pro Ala Leu Gly Leu Pro Trp Pro Ala Asp Leu Glu Val Val
 2115 2120 2125 2130

ctc tcc gac cgc gac acg gtg gcc gtg gac ctg gag acc gcc agg cgg 8096
 Leu Ser Asp Arg Asp Thr Val Ala Val Asp Leu Glu Thr Ala Arg Arg
 2135 2140 2145

cga ggg atg ctg ccc gac tac gcc gac tgc ctc ggc gag gag ccc gcc 8144
 Arg Gly Met Leu Pro Asp Tyr Ala Asp Cys Leu Gly Glu Glu Pro Ala
 2150 2155 2160

agc acc ggc agg tgac 8160
 Ser Thr Gly Arg
 2165

<210> 7
 <211> 322
 <212> PRT
 <213> Saccharopolyspora erythraea

<400> 7
 Met Asn Gly Ile Ser Asp Ser Pro Arg Gln Leu Ile Thr Leu Leu Gly
 1 5 10 15
 Ala Ser Gly Phe Val Gly Ser Ala Val Leu Arg Glu Leu Arg Asp His
 20 25 30
 Pro Val Arg Leu Arg Ala Val Ser Arg Gly Gly Ala Pro Ala Val Pro
 35 40 45
 Pro Gly Ala Ala Glu Val Glu Asp Leu Arg Ala Asp Leu Leu Glu Pro
 50 55 60
 Gly Arg Ala Ala Ala Ala Ile Glu Asp Ala Asp Val Ile Val His Leu
 65 70 75 80

Leu Val Pro Leu Ala Trp Ala Leu Arg Thr Ala Gly His Asp Val Arg
 20 25 30
 Val Ala Ala Gln Pro Ala Leu Thr Asp Ala Val Ile Gly Ala Gly Leu
 35 40 45
 Thr Ala Val Pro Val Gly Ser Asp His Arg Leu Phe Asp Ile Val Pro
 50 55 60
 Glu Val Ala Ala Gln Val His Arg Tyr Ser Phe Tyr Leu Asp Phe Tyr
 65 70 75 80
 His Arg Glu Gln Glu Leu His Ser Trp Glu Phe Leu Leu Gly Met Gln
 85 90 95
 Glu Ala Thr Ser Arg Trp Val Tyr Pro Val Val Asn Asn Asp Ser Phe
 100 105 110
 Val Ala Glu Leu Val Asp Phe Ala Arg Asp Trp Arg Pro Asp Leu Val
 115 120 125
 Leu Trp Glu Pro Phe Thr Phe Ala Gly Ala Val Ala Ala Arg Ala Cys
 130 135 140
 Gly Ala Ala His Ala Arg Leu Leu Trp Gly Ser Asp Leu Thr Gly Tyr
 145 150 155 160
 Phe Arg Gly Arg Phe Gln Ala Gln Arg Leu Arg Arg Pro Pro Glu Asp
 165 170 175
 Arg Pro Asp Pro Leu Gly Thr Trp Leu Thr Glu Val Ala Gly Arg Phe
 180 185 190
 Gly Val Glu Phe Gly Glu Asp Leu Ala Val Gly Gln Trp Ser Val Asp
 195 200 205
 Gln Leu Pro Pro Ser Phe Arg Leu Asp Thr Gly Met Glu Thr Val Val
 210 215 220
 Ala Arg Thr Leu Pro Tyr Asn Gly Ala Ser Val Val Pro Asp Trp Leu
 225 230 235 240
 Lys Lys Gly Ser Ala Thr Arg Arg Ile Cys Ile Thr Gly Gly Phe Ser
 245 250 255
 Gly Leu Gly Leu Ala Ala Asp Ala Asp Gln Phe Ala Arg Thr Leu Ala
 260 265 270
 Gln Leu Ala Arg Phe Asp Gly Glu Ile Val Val Thr Gly Ser Gly Pro
 275 280 285
 Asp Thr Ser Ala Val Pro Asp Asn Ile Arg Leu Val Asp Phe Val Pro
 290 295 300
 Met Gly Val Leu Leu Gln Asn Cys Ala Ala Ile Ile His His Gly Gly
 305 310 315 320

Ala Gly Thr Trp Ala Thr Ala Leu His His Gly Ile Pro Gln Ile Ser
325 330 335

Val Ala His Glu Trp Asp Cys Met Leu Arg Gly Gln Gln Thr Ala Glu
340 345 350

Leu Gly Ala Gly Ile Tyr Leu Arg Pro Asp Glu Val Asp Ala Asp Ser
355 360 365

Leu Ala Ser Ala Leu Thr Gln Val Val Glu Asp Pro Thr Tyr Thr Glu
370 375 380

Asn Ala Val Lys Leu Arg Glu Glu Ala Leu Ser Asp Pro Thr Pro Gln
385 390 395 400

Glu Ile Val Pro Arg Leu Glu Glu Leu Thr Arg Arg His Ala Gly
405 410 415

<210> 9

<211> 237

<212> PRT

<213> Saccharopolyspora erythraea

<400> 9

Met Tyr Glu Gly Gly Phe Ala Glu Leu Tyr Asp Arg Phe Tyr Arg Gly
1 5 10 15

Arg Gly Lys Asp Tyr Ala Ala Glu Ala Ala Gln Val Ala Arg Leu Val
20 25 30

Arg Asp Arg Leu Pro Ser Ala Ser Ser Leu Leu Asp Val Ala Cys Gly
35 40 45

Thr Gly Thr His Leu Arg Arg Phe Ala Asp Leu Phe Asp Asp Val Thr
50 55 60

Gly Leu Glu Leu Ser Ala Ala Met Ile Glu Val Ala Arg Pro Gln Leu
65 70 75 80

Gly Gly Ile Pro Val Leu Gln Gly Asp Met Arg Asp Phe Ala Leu Asp
85 90 95

Arg Glu Phe Asp Ala Val Thr Cys Met Phe Ser Ser Ile Gly His Met
100 105 110

Arg Asp Gly Ala Glu Leu Asp Gln Ala Leu Ala Ser Phe Ala Arg His
115 120 125

Leu Ala Pro Gly Gly Val Val Val Val Glu Pro Trp Trp Phe Pro Glu
130 135 140

Asp Phe Leu Asp Gly Tyr Val Ala Gly Asp Val Val Arg Asp Gly Asp
145 150 155 160

Leu Thr Ile Ser Arg Val Ser His Ser Val Arg Ala Gly Gly Ala Thr
165 170 175

Arg Met Glu Ile His Trp Val Val Ala Asp Ala Val Asn Gly Pro Arg
 180 185 190

His His Val Glu His Tyr Glu Ile Thr Leu Phe Glu Arg Gln Gln Tyr
 195 200 205

Glu Lys Ala Phe Thr Ala Ala Gly Cys Ala Val Gln Tyr Leu Glu Gly
 210 215 220

Gly Pro Ser Gly Arg Gly Leu Phe Val Gly Val Arg Gly
 225 230 235

<210> 10

<211> 510

<212> PRT

<213> Saccharopolyspora erythraea

<400> 10

Met Arg Val Leu Ile Asp Asn Ala Arg Arg Gln Gln Ala Glu Pro Ser
 1 5 10 15

Thr Thr Pro Gln Gly Glu Ser Met Gly Asp Arg Thr Gly Asp Arg Thr
 20 25 30

Ile Pro Glu Ser Ser Gln Thr Ala Thr Arg Phe Leu Leu Gly Asp Gly
 35 40 45

Gly Ile Pro Thr Ala Thr Ala Glu Thr His Asp Trp Leu Thr Arg Asn
 50 55 60

Gly Ala Glu Gln Arg Leu Glu Val Ala Arg Val Pro Phe Ser Ala Met
 65 70 75 80

Asp Arg Trp Ser Phe Gln Pro Glu Asp Gly Arg Leu Ala His Glu Ser
 85 90 95

Gly Arg Phe Phe Ser Ile Glu Gly Leu His Val Arg Thr Asn Phe Gly
 100 105 110

Trp Arg Arg Asp Trp Ile Gln Pro Ile Ile Val Gln Pro Glu Ile Gly
 115 120 125

Phe Leu Gly Leu Ile Val Lys Glu Phe Asp Gly Val Leu His Val Leu
 130 135 140

Ala Gln Ala Lys Ala Glu Pro Gly Asn Ile Asn Ala Val Gln Leu Ser
 145 150 155 160

Pro Thr Leu Gln Ala Thr Arg Ser Asn Tyr Thr Gly Val His Arg Gly
 165 170 175

Ser Lys Val Arg Phe Ile Glu Tyr Phe Asn Gly Thr Arg Pro Ser Arg
 180 185 190

Ile Leu Val Asp Val Leu Gln Ser Glu Gln Gly Ala Trp Phe Leu Arg

195	200	205
Lys Arg Asn Arg Asn Met Val Val Glu Val Phe Asp Asp Leu Pro Glu 210 215 220		
His Pro Asn Phe Arg Trp Leu Thr Val Ala Gln Leu Arg Ala Met Leu 225 230 235 240		
His His Asp Asn Val Val Asn Met Asp Leu Arg Thr Val Leu Ala Cys 245 250 255		
Val Pro Thr Ala Val Glu Arg Asp Arg Ala Asp Asp Val Leu Ala Arg 260 265 270		
Leu Pro Glu Gly Ser Phe Gln Ala Arg Leu Leu His Ser Phe Ile Gly 275 280 285		
Ala Gly Thr Pro Ala Asn Asn Met Asn Ser Leu Leu Ser Trp Ile Ser 290 295 300		
Asp Val Arg Ala Arg Arg Glu Phe Val Gln Arg Gly Arg Pro Leu Pro 305 310 315 320		
Asp Ile Glu Arg Ser Gly Trp Ile Arg Arg Asp Asp Gly Ile Glu His 325 330 335		
Glu Glu Lys Lys Tyr Phe Asp Val Phe Gly Val Thr Val Ala Thr Ser 340 345 350		
Asp Arg Glu Val Asn Ser Trp Met Gln Pro Leu Leu Ser Pro Ala Asn 355 360 365		
Asn Gly Leu Leu Ala Leu Leu Val Lys Asp Ile Gly Gly Thr Leu His 370 375 380		
Ala Leu Val Gln Leu Arg Thr Glu Ala Gly Gly Met Asp Val Ala Glu 385 390 395 400		
Leu Ala Pro Thr Val His Cys Gln Pro Asp Asn Tyr Ala Asp Ala Pro 405 410 415		
Glu Glu Phe Arg Pro Ala Tyr Val Asp Tyr Val Leu Asn Val Pro Arg 420 425 430		
Ser Gln Val Arg Tyr Asp Ala Trp His Ser Glu Glu Gly Gly Arg Phe 435 440 445		
Tyr Arg Asn Glu Asn Arg Tyr Met Leu Ile Glu Val Pro Ala Asp Phe 450 455 460		
Asp Ala Ser Ala Ala Pro Asp His Arg Trp Met Thr Phe Asp Gln Ile 465 470 475 480		
Thr Tyr Leu Leu Gly His Ser His Tyr Val Asn Ile Gln Leu Arg Ser 485 490 495		
Ile Ile Ala Cys Ala Ser Ala Val Tyr Thr Arg Thr Ala Gly		

500

505

510

<210> 11

<211> 489

<212> PRT

<213> Saccharopolyspora erythraea

<400> 11

Met Asn Thr Thr Arg Thr Ala Thr Ala Gln Glu Ala Gly Val Ala Asp
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Ala Ala Arg Pro Asp Val Asp Arg Arg Ala Val Val Arg Ala Leu Ser
 20 25 30

Ser Glu Val Ser Arg Val Thr Gly Ala Gly Asp Gly Asp Ala Asp Val
 35 40 45

Gln Ala Ala Arg Leu Ala Asp Leu Ala Ala His Tyr Gly Ala His Pro
 50 55 60

Phe Thr Pro Leu Glu Gln Thr Arg Ala Arg Leu Gly Leu Asp Arg Ala
 65 70 75 80

Glu Phe Ala His Leu Leu Asp Leu Phe Gly Arg Ile Pro Asp Leu Gly
 85 90 95

Thr Ala Val Glu His Gly Pro Ala Gly Lys Tyr Trp Ser Asn Thr Ile
 100 105 110

Lys Pro Leu Asp Ala Ala Gly Ala Leu Asp Ala Ala Val Tyr Arg Lys
 115 120 125

Pro Ala Phe Pro Tyr Ser Val Gly Leu Tyr Pro Gly Pro Thr Cys Met
 130 135 140

Phe Arg Cys His Phe Cys Val Arg Val Thr Gly Ala Arg Tyr Glu Ala
 145 150 155 160

Ala Ser Val Pro Ala Gly Asn Glu Thr Leu Ala Ala Ile Ile Asp Glu
 165 170 175

Val Pro Thr Asp Asn Pro Lys Ala Met Tyr Met Ser Gly Gly Leu Glu
 180 185 190

Pro Leu Thr Asn Pro Gly Leu Gly Glu Leu Val Ser His Ala Ala Gly
 195 200 205

Arg Gly Phe Asp Leu Thr Val Tyr Thr Asn Ala Phe Ala Leu Thr Glu
 210 215 220

Gln Thr Leu Asn Arg Gln Pro Gly Leu Trp Glu Leu Gly Ala Ile Arg
 225 230 235 240

Thr Ser Leu Tyr Gly Leu Asn Asn Asp Glu Tyr Glu Thr Thr Thr Gly
 245 250 255

Lys Arg Gly Ala Phe Glu Arg Val Lys Lys Asn Leu Gln Gly Phe Leu

260										265										270										
Arg	Met	Arg	Ala	Glu	Arg	Asp	Ala	Pro	Ile	Arg	Leu	Gly	Phe	Asn	His															
		275					280					285																		
Ile	Ile	Leu	Pro	Gly	Arg	Ala	Asp	Arg	Leu	Thr	Asp	Leu	Val	Asp	Phe															
	290					295					300																			
Ile	Ala	Glu	Leu	Asn	Glu	Ser	Ser	Pro	Gln	Arg	Pro	Leu	Asp	Phe	Val															
305				310					315						320															
Thr	Val	Arg	Glu	Asp	Tyr	Ser	Gly	Arg	Asp	Asp	Gly	Arg	Leu	Ser	Asp															
			325					330					335																	
Ser	Glu	Arg	Asn	Glu	Leu	Arg	Glu	Gly	Leu	Val	Arg	Phe	Val	Asp	Tyr															
			340					345					350																	
Ala	Ala	Glu	Arg	Thr	Pro	Gly	Met	His	Ile	Asp	Leu	Gly	Tyr	Ala	Leu															
	355					360						365																		
Glu	Ser	Leu	Arg	Arg	Gly	Val	Asp	Ala	Glu	Leu	Leu	Arg	Ile	Arg	Pro															
	370				375						380																			
Glu	Thr	Met	Arg	Pro	Thr	Ala	His	Pro	Gln	Val	Ala	Val	Gln	Ile	Asp															
385					390				395					400																
Leu	Leu	Gly	Asp	Val	Tyr	Leu	Tyr	Arg	Glu	Ala	Gly	Phe	Pro	Glu	Leu															
			405					410					415																	
Glu	Gly	Ala	Thr	Arg	Tyr	Ile	Ala	Gly	Arg	Val	Thr	Pro	Ser	Thr	Ser															
		420					425					430																		
Leu	Arg	Glu	Val	Val	Glu	Asn	Phe	Val	Leu	Glu	Asn	Glu	Gly	Val	Gln															
	435					440					445																			
Pro	Arg	Pro	Gly	Asp	Glu	Tyr	Phe	Leu	Asp	Gly	Phe	Asp	Gln	Ser	Val															
	450				455						460																			
Thr	Ala	Arg	Leu	Asn	Gln	Leu	Glu	Arg	Asp	Ile	Ala	Asp	Gly	Trp	Glu															
465				470				475						480																
Asp	His	Arg	Gly	Phe	Leu	Arg	Gly	Arg																						
			485																											

<210> 12
 <211> 193
 <212> PRT
 <213> Saccharopolyspora erythraea

<400> 12
 Met Ala Gly Gly Phe Glu Phe Thr Pro Asp Pro Lys Gln Asp Arg Arg
 1 5 10 15
 Gly Leu Phe Val Ser Pro Leu Gln Asp Glu Ala Phe Val Gly Ala Val
 20 25 30

Gly His Arg Phe Pro Val Ala Gln Met Asn His Ile Val Ser Ala Arg
 35 40 45
 Gly Val Leu Arg Gly Leu His Phe Thr Thr Thr Pro Pro Gly Gln Cys
 50 55 60
 Lys Tyr Val Tyr Cys Ala Arg Gly Arg Ala Leu Asp Val Ile Val Asp
 65 70 75 80
 Ile Arg Val Gly Ser Pro Thr Phe Gly Lys Trp Asp Ala Val Glu Met
 85 90 95
 Asp Thr Glu His Phe Arg Ala Val Tyr Phe Pro Arg Gly Thr Ala His
 100 105 110
 Ala Phe Leu Ala Leu Glu Asp Asp Thr Leu Met Ser Tyr Leu Val Ser
 115 120 125
 Thr Pro Tyr Val Ala Glu Tyr Glu Gln Ala Ile Asp Pro Phe Asp Pro
 130 135 140
 Ala Leu Gly Leu Pro Trp Pro Ala Asp Leu Glu Val Val Leu Ser Asp
 145 150 155 160
 Arg Asp Thr Val Ala Val Asp Leu Glu Thr Ala Arg Arg Arg Gly Met
 165 170 175
 Leu Pro Asp Tyr Ala Asp Cys Leu Gly Glu Glu Pro Ala Ser Thr Gly
 180 185 190

Arg

<210> 13
 <211> 1206
 <212> DNA
 <213> Saccharopolyspora erythraea

<220>
 <221> CDS
 <222> (1)..(1203)
 <223> /function= "involved in the biosynthesis of
 desosamine" /gene= "eryCIV" /note= "SEQ ID No 6
 from 4837 to 6039"

<220>
 <221> mat_peptide
 <222> (1)

<400> 131
 atg aaa cgc gcg ctg acc gac ctg gcg atc ttc ggc ggc ccc gag gca 48
 Met Lys Arg Ala Leu Thr Asp Leu Ala Ile Phe Gly Gly Pro Glu Ala
 1 5 10 15
 ttc ctg cac acc ctc tac gtg ggc agg ccg acc gtc ggg gac cgg gag 96
 Phe Leu His Thr Leu Tyr Val Gly Arg Pro Thr Val Gly Asp Arg Glu
 20 25 30

cgg ttc ttc gcc cgc ctg gag tgg gcg ctg aac aac aac tgg ctg acc Arg Phe Phe Ala Arg Leu Glu Trp Ala Leu Asn Asn Asn Trp Leu Thr 35 40 45	144
aac ggc gga cca ctg gtg cgc gag ttc gag ggc cgg gtc gcc gac ctg Asn Gly Gly Pro Leu Val Arg Glu Phe Glu Gly Arg Val Ala Asp Leu 50 55 60	192
gcg ggt gtc cgc cac tgc gtg gcc acc tgc aac gcg acg gtc gcg ctg Ala Gly Val Arg His Cys Val Ala Thr Cys Asn Ala Thr Val Ala Leu 65 70 75 80	240
caa ctg gtg ctg cgc gcg agc gac gtg tcc ggc gag gtc gtc atg cct Gln Leu Val Leu Arg Ala Ser Asp Val Ser Gly Glu Val Val Met Pro 85 90 95	288
tcg atg acg ttc gcg gcc acc gcg cac gcg gcg agc tgg ctg ggg ctg Ser Met Thr Phe Ala Ala Thr Ala His Ala Ala Ser Trp Leu Gly Leu 100 105 110	336
gaa ccg gtg ttc tgc gac gtg gac ccc gag acc ggc ctg ctc gac ccc Glu Pro Val Phe Cys Asp Val Asp Pro Glu Thr Gly Leu Leu Asp Pro 115 120 125	384
gag cac gtc gcg tcg ctg gtg aca ccg cgg acg ggc gcg atc atc ggc Glu His Val Ala Ser Leu Val Thr Pro Arg Thr Gly Ala Ile Ile Gly 130 135 140	432
gtg cac ctg tgg ggc agg ccc gct ccg gtc gag gcg ctg gag aag atc Val His Leu Trp Gly Arg Pro Ala Pro Val Glu Ala Leu Glu Lys Ile 145 150 155 160	480
gcc gcc gag cac cag gtc aaa ctc ttc ttc gac gcc gcg cac gcg ctg Ala Ala Glu His Gln Val Lys Leu Phe Phe Asp Ala Ala His Ala Leu 165 170 175	528
ggc tgc acc gcc ggc ggg cgg ccg gtc ggc gcc ttc ggc aac gcc gag Gly Cys Thr Ala Gly Gly Arg Pro Val Gly Ala Phe Gly Asn Ala Glu 180 185 190	576
gtg ttc agc ttc cac gcc acg aag gcg gtc acc tcg ttc gag ggc ggc Val Phe Ser Phe His Ala Thr Lys Ala Val Thr Ser Phe Glu Gly Gly 195 200 205	624
gcc atc gtc acc gac gac ggg ctg ctg gcc gac cgc atc cgc gcc atg Ala Ile Val Thr Asp Asp Gly Leu Leu Ala Asp Arg Ile Arg Ala Met 210 215 220	672
cac aac ttc ggg atc gca ccg gac aag ctg gtg acc gat gtc ggc acc His Asn Phe Gly Ile Ala Pro Asp Lys Leu Val Thr Asp Val Gly Thr 225 230 235 240	720
aac ggc aag atg agc gag tgc gcc gcg gcg atg ggc ctc acc tcg ctc Asn Gly Lys Met Ser Glu Cys Ala Ala Ala Met Gly Leu Thr Ser Leu 245 250 255	768

gac gcc ttc gcc gag acc agg gtg cac aac cgc ctc aac cac gcg ctc	816
Asp Ala Phe Ala Glu Thr Arg Val His Asn Arg Leu Asn His Ala Leu	
260 265 270	
tac tcc gac gag ctc cgc gac gtg cgc ggc ata tcc gtg cac gcg ttc	864
Tyr Ser Asp Glu Leu Arg Asp Val Arg Gly Ile Ser Val His Ala Phe	
275 280 285	
gat cct ggc gag cag aac aac tac cag tac gtg atc atc tcg gtg gac	912
Asp Pro Gly Glu Gln Asn Asn Tyr Gln Tyr Val Ile Ile Ser Val Asp	
290 295 300	
tcc gcg gcc acc ggc atc gac cgc gac cag ttg cag gcg atc ctg cga	960
Ser Ala Ala Thr Gly Ile Asp Arg Asp Gln Leu Gln Ala Ile Leu Arg	
305 310 315 320	
gcg gag aag gtt gtg gca caa ccc tac ttc tcc ccc ggg tgc cac cag	1008
Ala Glu Lys Val Val Ala Gln Pro Tyr Phe Ser Pro Gly Cys His Gln	
325 330 335	
atg cag ccg tac cgg acc gag ccg ccg ctg cgg ctg gag aac acc gaa	1056
Met Gln Pro Tyr Arg Thr Glu Pro Pro Leu Arg Leu Glu Asn Thr Glu	
340 345 350	
cag ctc tcc gac cgg gtg ctc gcg ctg ccc acc ggc ccc gcg gtg tcc	1104
Gln Leu Ser Asp Arg Val Leu Ala Leu Pro Thr Gly Pro Ala Val Ser	
355 360 365	
agc gag gac atc cgg cgg gtg tgc gac atc atc cgg ctc gcc gcc acc	1152
Ser Glu Asp Ile Arg Arg Val Cys Asp Ile Ile Arg Leu Ala Ala Thr	
370 375 380	
agc ggc gag ctg atc aac gcg caa tgg gac cag agg acg cgc aac ggt	1200
Ser Gly Glu Leu Ile Asn Ala Gln Trp Asp Gln Arg Thr Arg Asn Gly	
385 390 395 400	
tcg tga	1206
Ser	

<210> 14

<211> 401

<212> PRT

<213> Saccharopolyspora erythraea

<400> 14

Met	Lys	Arg	Ala	Leu	Thr	Asp	Leu	Ala	Ile	Phe	Gly	Gly	Pro	Glu	Ala
1				5					10					15	

Phe	Leu	His	Thr	Leu	Tyr	Val	Gly	Arg	Pro	Thr	Val	Gly	Asp	Arg	Glu
		20						25					30		

Arg	Phe	Phe	Ala	Arg	Leu	Glu	Trp	Ala	Leu	Asn	Asn	Asn	Trp	Leu	Thr
		35					40					45			

Asn	Gly	Gly	Pro	Leu	Val	Arg	Glu	Phe	Glu	Gly	Arg	Val	Ala	Asp	Leu
	50					55					60				

Ala	Gly	Val	Arg	His	Cys	Val	Ala	Thr	Cys	Asn	Ala	Thr	Val	Ala	Leu	65	70	75	80
Gln	Leu	Val	Leu	Arg	Ala	Ser	Asp	Val	Ser	Gly	Glu	Val	Val	Met	Pro	85	90	95	
Ser	Met	Thr	Phe	Ala	Ala	Thr	Ala	His	Ala	Ala	Ser	Trp	Leu	Gly	Leu	100	105	110	
Glu	Pro	Val	Phe	Cys	Asp	Val	Asp	Pro	Glu	Thr	Gly	Leu	Leu	Asp	Pro	115	120	125	
Glu	His	Val	Ala	Ser	Leu	Val	Thr	Pro	Arg	Thr	Gly	Ala	Ile	Ile	Gly	130	135	140	
Val	His	Leu	Trp	Gly	Arg	Pro	Ala	Pro	Val	Glu	Ala	Leu	Glu	Lys	Ile	145	150	155	160
Ala	Ala	Glu	His	Gln	Val	Lys	Leu	Phe	Phe	Asp	Ala	Ala	His	Ala	Leu	165	170	175	
Gly	Cys	Thr	Ala	Gly	Gly	Arg	Pro	Val	Gly	Ala	Phe	Gly	Asn	Ala	Glu	180	185	190	
Val	Phe	Ser	Phe	His	Ala	Thr	Lys	Ala	Val	Thr	Ser	Phe	Glu	Gly	Gly	195	200	205	
Ala	Ile	Val	Thr	Asp	Asp	Gly	Leu	Leu	Ala	Asp	Arg	Ile	Arg	Ala	Met	210	215	220	
His	Asn	Phe	Gly	Ile	Ala	Pro	Asp	Lys	Leu	Val	Thr	Asp	Val	Gly	Thr	225	230	235	240
Asn	Gly	Lys	Met	Ser	Glu	Cys	Ala	Ala	Ala	Met	Gly	Leu	Thr	Ser	Leu	245	250	255	
Asp	Ala	Phe	Ala	Glu	Thr	Arg	Val	His	Asn	Arg	Leu	Asn	His	Ala	Leu	260	265	270	
Tyr	Ser	Asp	Glu	Leu	Arg	Asp	Val	Arg	Gly	Ile	Ser	Val	His	Ala	Phe	275	280	285	
Asp	Pro	Gly	Glu	Gln	Asn	Asn	Tyr	Gln	Tyr	Val	Ile	Ile	Ser	Val	Asp	290	295	300	
Ser	Ala	Ala	Thr	Gly	Ile	Asp	Arg	Asp	Gln	Leu	Gln	Ala	Ile	Leu	Arg	305	310	315	320
Ala	Glu	Lys	Val	Val	Ala	Gln	Pro	Tyr	Phe	Ser	Pro	Gly	Cys	His	Gln	325	330	335	
Met	Gln	Pro	Tyr	Arg	Thr	Glu	Pro	Pro	Leu	Arg	Leu	Glu	Asn	Thr	Glu	340	345	350	
Gln	Leu	Ser	Asp	Arg	Val	Leu	Ala	Leu	Pro	Thr	Gly	Pro	Ala	Val	Ser	355	360	365	

Ser Glu Asp Ile Arg Arg Val Cys Asp Ile Ile Arg Leu Ala Ala Thr
 370 375 380

Ser Gly Glu Leu Ile Asn Ala Gln Trp Asp Gln Arg Thr Arg Asn Gly
 385 390 395 400

Ser

<210> 15
 <211> 6093
 <212> DNA
 <213> Streptomyces antibioticus

<220>
 <221> CDS
 <222> (184)..(1386)
 <223> /gene= "oleP1"

<220>
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 <222> (1437)..(2714)
 <223> /function= "glycosylation of 8,
 8a-desoxyoleandolide" /gene= "oleG1"
 /transl_except= (pos: 1437...1439, aa: Met)

<220>
 <221> CDS
 <222> (2722)..(3999)
 <223> /function= "glycosylation of 8,
 8a-desoxyoleandolide" /gene= "oleG2"

<220>
 <221> CDS
 <222> (4810)..(5967)
 <223> /gene= "oleY"

<220>
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Cys Gly Met Glu Asp Asp Pro Ser Pro Phe Tyr Asp Ala Ile Arg Thr	
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 Leu Pro Asp Thr Phe Asp Leu Val Glu Glu Tyr Ala Gly Leu Val Pro
 145 150 155 160
 Val Glu Val Leu Ala Arg Ile Trp Gly Val Pro Glu Glu Asp Arg Ala
 165 170 175
 Arg Phe Gly Arg Asp Cys Arg Ala Leu Ala Pro Ala Leu Asp Ser Leu
 180 185 190
 Leu Cys Pro Gln Gln Leu Ala Leu Ser Lys Asp Met Ala Ser Ala Leu
 195 200 205
 Glu Asp Leu Arg Leu Leu Phe Asp Gly Leu Asp Ala Thr Pro Arg Leu
 210 215 220
 Ala Gly Pro Ala Asp Gly Asp Gly Thr Ala Val Ala Met Leu Thr Val
 225 230 235 240
 Leu Leu Cys Thr Glu Pro Val Thr Thr Ala Ile Gly Asn Thr Val Leu
 245 250 255
 Gly Leu Leu Pro Gly Gln Trp Pro Val Pro Cys Thr Gly Arg Val Ala
 260 265 270
 Ala Gly Gln Val Ala Gly Gln Ala Leu His Arg Ala Val Ser Tyr Arg
 275 280 285
 Ile Ala Thr Arg Phe Ala Arg Glu Asp Leu Glu Leu Ala Gly Cys Glu
 290 295 300
 Val Lys Ser Gly Asp Glu Val Val Val Leu Ala Gly Ala Ile Gly Arg
 305 310 315 320
 Asn Gly Pro Ser Ala Ala Ala Pro Pro Ala Pro Pro Gly Pro Ala Ala
 325 330 335
 Pro Pro Ala Pro Ser Val Phe Gly Ala Ala Ala Phe Glu Asn Ala Leu
 340 345 350

Ala Glu Pro Leu Val Arg Ala Val Thr Gly Ala Ala Leu Gln Ala Leu
 355 360 365

Ala Glu Gly Pro Pro Arg Leu Thr Ala Ala Gly Pro Val Val Arg Arg
 370 375 380

Arg Arg Ser Pro Val Val Gly Gly Leu His Arg Ala Pro Val Ala Ala
 385 390 395 400

Ala

<210> 17

<211> 426

<212> PRT

<213> Streptomyces antibioticus

<400> 17

Met Met Met Thr Thr Phe Ala Ala Asn Thr His Phe Gln Pro Leu Val
 1 5 10 15

Pro Leu Ala Trp Ala Leu Arg Thr Ala Gly His Glu Val Arg Val Val
 20 25 30

Ser Gln Pro Ser Leu Ser Asp Val Val Thr Gln Ala Gly Leu Thr Ser
 35 40 45

Val Pro Val Gly Thr Glu Ala Pro Val Glu Gln Phe Ala Ala Thr Trp
 50 55 60

Gly Asp Asp Ala Tyr Ile Gly Val Asn Ser Ile Asp Phe Thr Gly Asn
 65 70 75 80

Asp Pro Gly Leu Trp Thr Trp Pro Tyr Leu Leu Gly Met Glu Thr Met
 85 90 95

Leu Val Pro Ala Phe Tyr Glu Leu Leu Asn Asn Glu Ser Phe Val Asp
 100 105 110

Gly Val Val Glu Phe Ala Arg Asp Trp Arg Pro Asp Leu Val Ile Trp
 115 120 125

Glu Pro Leu Thr Phe Ala Gly Ala Val Ala Ala Arg Val Thr Gly Ala
 130 135 140

Ala His Ala Arg Leu Pro Trp Gly Gln Glu Ile Thr Leu Arg Gly Arg
 145 150 155 160

Gln Ala Phe Leu Ala Glu Arg Ala Leu Gln Pro Phe Glu His Arg Glu
 165 170 175

Asp Pro Thr Ala Glu Trp Leu Gly Arg Met Leu Asp Arg Tyr Gly Cys
 180 185 190

Ser Phe Asp Glu Glu Met Val Thr Gly Gln Trp Thr Ile Asp Thr Leu
 195 200 205

Pro Arg Ser Met Arg Leu Glu Leu Ser Glu Glu Leu Arg Thr Leu Asp
 210 215 220
 Met Arg Tyr Val Pro Tyr Asn Gly Pro Ala Val Val Pro Pro Trp Val
 225 230 235 240
 Trp Glu Pro Cys Glu Arg Pro Arg Val Cys Leu Thr Ile Gly Thr Ser
 245 250 255
 Gln Arg Asp Ser Gly Arg Asp His Val Pro Leu Asp His Leu Leu Asp
 260 265 270
 Ser Leu Ala Asp Val Asp Ala Glu Ile Val Ala Thr Leu Asp Thr Thr
 275 280 285
 Gln Gln Glu Arg Leu Arg Gly Ala Ala Pro Gly Asn Val Arg Leu Val
 290 295 300
 Asp Phe Val Pro Leu His Ala Leu Met Pro Thr Cys Ser Ala Ile Val
 305 310 315 320
 His His Gly Gly Pro Gly Thr Trp Ser Thr Ala Ala Leu His Gly Val
 325 330 335
 Pro Gln Ile Ile Leu Asp Thr Ser Trp Asp Thr Pro Val Arg Ala Gln
 340 345 350
 Arg Met Gln Gln Leu Gly Ala Gly Leu Ser Met Pro Val Gly Glu Leu
 355 360 365
 Gly Val Glu Ala Leu Arg Asp Arg Val Leu Arg Leu Leu Gly Glu Pro
 370 375 380
 Glu Phe Arg Ala Gly Ala Glu Arg Ile Arg Ala Glu Met Leu Ala Met
 385 390 395 400
 Pro Ala Pro Gly Asp Val Val Pro Asp Leu Glu Arg Leu Thr Ala Glu
 405 410 415
 His Ala Thr Gly Ala Met Ala Gly Arg Arg
 420 425

<210> 18

<211> 426

<212> PRT

<213> Streptomyces antibioticus

<400> 18

Met Arg Val Leu Leu Thr Cys Phe Ala Asn Asp Thr His Phe His Gly
 1 5 10 15

Leu Val Pro Leu Ala Trp Ala Leu Arg Ala Ala Gly His Glu Val Arg
 20 25 30

Val Ala Ser Gln Pro Ala Leu Ser Asp Thr Ile Thr Gln Ala Gly Leu

35					40					45					
Thr	Ala	Val	Pro	Val	Gly	Arg	Asp	Thr	Ala	Phe	Leu	Glu	Leu	Met	Gly
50						55					60				
Glu	Ile	Gly	Ala	Asp	Val	Gln	Lys	Tyr	Ser	Thr	Gly	Ile	Asp	Leu	Gly
65					70					75					80
Val	Arg	Ala	Glu	Leu	Thr	Ser	Trp	Glu	Tyr	Leu	Leu	Gly	Met	His	Thr
				85					90					95	
Thr	Leu	Val	Pro	Thr	Phe	Tyr	Ser	Leu	Val	Asn	Asp	Glu	Pro	Phe	Val
			100					105					110		
Asp	Gly	Leu	Val	Ala	Leu	Thr	Arg	Ala	Trp	Arg	Pro	Asp	Leu	Ile	Leu
		115					120					125			
Trp	Glu	His	Phe	Ser	Phe	Ala	Gly	Ala	Leu	Ala	Ala	Arg	Ala	Thr	Gly
	130					135						140			
Thr	Pro	His	Ala	Arg	Val	Leu	Trp	Gly	Ser	Asp	Leu	Ile	Val	Arg	Phe
145					150					155					160
Arg	Arg	Asp	Phe	Leu	Ala	Glu	Arg	Ala	Asn	Arg	Pro	Ala	Glu	His	Arg
				165					170					175	
Glu	Asp	Pro	Met	Ala	Glu	Trp	Leu	Gly	Trp	Ala	Ala	Glu	Arg	Leu	Gly
			180					185					190		
Ser	Thr	Phe	Asp	Glu	Glu	Leu	Val	Thr	Gly	Gln	Trp	Thr	Ile	Asp	Pro
		195					200						205		
Leu	Pro	Arg	Ser	Met	Arg	Leu	Pro	Thr	Gly	Thr	Thr	Thr	Val	Pro	Met
	210					215					220				
Arg	Tyr	Val	Pro	Tyr	Asn	Gly	Arg	Ala	Val	Val	Pro	Ala	Trp	Val	Arg
225					230					235					240
Gln	Arg	Ala	Arg	Arg	Pro	Arg	Ile	Cys	Leu	Thr	Leu	Gly	Val	Ser	Ala
				245					250					255	
Arg	Gln	Thr	Leu	Gly	Asp	Gly	Val	Ser	Leu	Ala	Glu	Val	Leu	Ala	Ala
			260					265					270		
Leu	Gly	Asp	Val	Asp	Ala	Glu	Ile	Val	Ala	Thr	Leu	Asp	Ala	Ser	Gln
		275					280					285			
Arg	Lys	Leu	Leu	Gly	Pro	Val	Pro	Asp	Asn	Val	Arg	Leu	Val	Asp	Phe
	290					295					300				
Val	Pro	Leu	His	Ala	Leu	Met	Pro	Thr	Cys	Ser	Ala	Ile	Val	His	His
305					310					315					320
Gly	Gly	Ala	Gly	Thr	Trp	Leu	Thr	Ala	Ala	Val	His	Gly	Val	Pro	Gln
				325					330					335	
Ile	Val	Leu	Gly	Asp	Leu	Trp	Asp	Asn	Leu	Leu	Arg	Ala	Arg	Gln	Thr

340 345 350
 Gln Ala Ala Gly Ala Gly Leu Phe Ile His Pro Ser Glu Val Thr Ala
 355 360 365
 Ala Gly Leu Gly Glu Gly Val Arg Arg Val Leu Thr Asp Pro Ser Ile
 370 375 380
 Arg Ala Ala Ala Gln Arg Val Arg Asp Glu Met Asn Ala Glu Pro Thr
 385 390 395 400
 Pro Gly Glu Val Val Thr Val Leu Glu Arg Leu Ala Ala Ser Gly Gly
 405 410 415
 Arg Gly Arg Gly Gly Gly Asn His Ala Gly
 420 425

<210> 19
 <211> 386
 <212> PRT
 <213> Streptomyces antibioticus

<400> 19
 Met Ser Tyr Asp Asp His Ala Val Leu Glu Ala Ile Leu Arg Cys Ala
 1 5 10 15
 Gly Gly Asp Glu Arg Phe Leu Leu Asn Thr Val Glu Glu Trp Gly Ala
 20 25 30
 Ala Glu Ile Thr Ala Ala Leu Val Asp Glu Leu Leu Phe Arg Cys Glu
 35 40 45
 Ile Pro Gln Val Gly Gly Glu Ala Phe Ile Gly Leu Asp Val Leu His
 50 55 60
 Gly Ala Asp Arg Ile Ser His Val Leu Gln Val Thr Asp Gly Lys Pro
 65 70 75 80
 Val Thr Ser Ala Glu Pro Ala Gly Gln Glu Leu Gly Gly Arg Thr Trp
 85 90 95
 Ser Ser Arg Ser Ala Thr Leu Leu Arg Glu Leu Phe Gly Pro Pro Ser
 100 105 110
 Gly Arg Thr Ala Gly Gly Phe Gly Val Ser Phe Leu Pro Asp Leu Arg
 115 120 125
 Gly Pro Arg Thr Met Glu Gly Ala Ala Leu Ala Ala Arg Ala Thr Asn
 130 135 140
 Val Val Leu His Ala Thr Thr Asn Glu Thr Pro Pro Leu Asp Arg Leu
 145 150 155 160
 Ala Leu Arg Tyr Glu Ser Asp Lys Trp Gly Gly Val His Trp Phe Thr
 165 170 175

Gly His Tyr Asp Arg His Leu Arg Ala Val Arg Asp Gln Ala Val Arg
 180 185 190
 Ile Leu Glu Ile Gly Ile Gly Gly Tyr Asp Asp Leu Leu Pro Ser Gly
 195 200 205
 Ala Ser Leu Lys Met Trp Lys Arg Tyr Phe Pro Arg Gly Leu Val Phe
 210 215 220
 Gly Val Asp Ile Phe Asp Ser Arg Arg Ala Thr Ser Arg Val Ser Arg
 225 230 235 240
 Arg Ser Ala Ala Arg Gln Asp Asp Pro Glu Phe Met Arg Arg Val Ala
 245 250 255
 Glu Glu His Gly Pro Phe Asp Val Ile Ile Asp Asp Gly Ser His Ile
 260 265 270
 Asn Ala His Met Arg Thr Ser Phe Ser Val Met Phe Pro His Leu Arg
 275 280 285
 Asn Gly Gly Phe Tyr Val Ile Glu Asp Thr Phe Thr Ser Tyr Trp Pro
 290 295 300
 Gly Tyr Gly Gly Pro Ser Gly Ala Arg Cys Pro Ser Gly Thr Thr Ala
 305 310 315 320
 Leu Glu Met Val Lys Gly Leu Ile Asp Ser Val His Tyr Glu Glu Arg
 325 330 335
 Pro Asp Gly Ala Ala Thr Ala Asp Tyr Ile Ala Arg Asn Leu Val Gly
 340 345 350
 Leu His Ala Tyr Gln Thr Thr Ser Ser Ser Arg Arg Ala Ile Asn
 355 360 365
 Lys Glu Gly Gly Ile Pro His Thr Val Pro Arg Glu Pro Phe Trp Asn
 370 375 380
 Asp Asn
 385

<210> 20
 <211> 738
 <212> DNA
 <213> Streptomyces antibioticus

<220>
 <221> CDS
 <222> (1)..(738)
 <223> /gene= "oleM" /note= "SEQ ID No. 15 from 3992 to
 4729"

<220>
 <221> mat_peptide
 <222> (1)

<400> 20
atg cgg gct gac acg gag ccg acc acc ggg tac gag gac gag ttc gcc 48
Met Arg Ala Asp Thr Glu Pro Thr Thr Gly Tyr Glu Asp Glu Phe Ala
1 5 10 15

gag atc tac gac gcc gtg tac ccg ggc ccg ggc aag gac tac gcc ggc 96
Glu Ile Tyr Asp Ala Val Tyr Arg Gly Arg Gly Lys Asp Tyr Ala Gly
20 25 30

gag gcg aag gac gtg gcg gac ctc gtg cgc gac ccg gtg ccg gac gcg 144
Glu Ala Lys Asp Val Ala Asp Leu Val Arg Asp Arg Val Pro Asp Ala
35 40 45

tcc tcc ctc ctg gac gtg gcc tgc ggc acg ggc gcg cac ctg ccg cac 192
Ser Ser Leu Leu Asp Val Ala Cys Gly Thr Gly Ala His Leu Arg His
50 55 60

ttc gcc acg ctc ttc gac gac gcc cgc ggt ctc gaa ctg tcc gcg agc 240
Phe Ala Thr Leu Phe Asp Asp Ala Arg Gly Leu Glu Leu Ser Ala Ser
65 70 75 80

atg ctg gac atc gcc cgc tcc cgc atg ccg ggc gtg ccg ctg cac caa 288
Met Leu Asp Ile Ala Arg Ser Arg Met Pro Gly Val Pro Leu His Gln
85 90 95

ggg gac atg cga tcc ttc gac ctg ggg cca cgc gtc tcc gcg gtc acc 336
Gly Asp Met Arg Ser Phe Asp Leu Gly Pro Arg Val Ser Ala Val Thr
100 105 110

tgc atg ttc agc tcc gtc ggc cac ctg gcc acc acc gcc gaa ctc gac 384
Cys Met Phe Ser Ser Val Gly His Leu Ala Thr Thr Ala Glu Leu Asp
115 120 125

gcg acg ctg ccg tgc ttc gcc ccg cac acc ccg ccc ggc ggc gtg gcc 432
Ala Thr Leu Arg Cys Phe Ala Arg His Thr Arg Pro Gly Gly Val Ala
130 135 140

gtc atc gaa ccg tgg tgg ttc ccg gag acc ttc acc gac ggc tac gtg 480
Val Ile Glu Pro Trp Trp Phe Pro Glu Thr Phe Thr Asp Gly Tyr Val
145 150 155 160

gcg ggt gac atc gta cgc gtc gac ggc ccg acc atc tcc ccg gtg tcc 528
Ala Gly Asp Ile Val Arg Val Asp Gly Arg Thr Ile Ser Arg Val Ser
165 170 175

cac tcg gta ccg gac ggc ggc gcc acc cgc atg gag atc cac tac gtg 576
His Ser Val Arg Asp Gly Gly Ala Thr Arg Met Glu Ile His Tyr Val
180 185 190

atc gcc gac gcc gag cac ggt ccc ccg cac ctg gtc gag cac cac cgc 624
Ile Ala Asp Ala Glu His Gly Pro Arg His Leu Val Glu His His Arg
195 200 205

atc acg ctg ttc ccg ccg cat gcg tac acg gcc gcg tac gag aag gcg 672
Ile Thr Leu Phe Pro Arg His Ala Tyr Thr Ala Ala Tyr Glu Lys Ala
210 215 220

ggc tac acc gtc gag tac ctc gac ggc ggg ccc tcg ggc cgg ggg ctg 720
 Gly Tyr Thr Val Glu Tyr Leu Asp Gly Gly Pro Ser Gly Arg Gly Leu
 225 230 235 240

ttc gtc ggc acc cgg acg 738
 Phe Val Gly Thr Arg Thr
 245

<210> 21
 <211> 246
 <212> PRT
 <213> Streptomyces antibioticus

<400> 21
 Met Arg Ala Asp Thr Glu Pro Thr Thr Gly Tyr Glu Asp Glu Phe Ala
 1 5 10 15
 Glu Ile Tyr Asp Ala Val Tyr Arg Gly Arg Gly Lys Asp Tyr Ala Gly
 20 25 30
 Glu Ala Lys Asp Val Ala Asp Leu Val Arg Asp Arg Val Pro Asp Ala
 35 40 45
 Ser Ser Leu Leu Asp Val Ala Cys Gly Thr Gly Ala His Leu Arg His
 50 55 60
 Phe Ala Thr Leu Phe Asp Asp Ala Arg Gly Leu Glu Leu Ser Ala Ser
 65 70 75 80
 Met Leu Asp Ile Ala Arg Ser Arg Met Pro Gly Val Pro Leu His Gln
 85 90 95
 Gly Asp Met Arg Ser Phe Asp Leu Gly Pro Arg Val Ser Ala Val Thr
 100 105 110
 Cys Met Phe Ser Ser Val Gly His Leu Ala Thr Thr Ala Glu Leu Asp
 115 120 125
 Ala Thr Leu Arg Cys Phe Ala Arg His Thr Arg Pro Gly Gly Val Ala
 130 135 140
 Val Ile Glu Pro Trp Trp Phe Pro Glu Thr Phe Thr Asp Gly Tyr Val
 145 150 155 160
 Ala Gly Asp Ile Val Arg Val Asp Gly Arg Thr Ile Ser Arg Val Ser
 165 170 175
 His Ser Val Arg Asp Gly Gly Ala Thr Arg Met Glu Ile His Tyr Val
 180 185 190
 Ile Ala Asp Ala Glu His Gly Pro Arg His Leu Val Glu His His Arg
 195 200 205
 Ile Thr Leu Phe Pro Arg His Ala Tyr Thr Ala Ala Tyr Glu Lys Ala
 210 215 220

Gly Tyr Thr Val Glu Tyr Leu Asp Gly Gly Pro Ser Gly Arg Gly Leu
225 230 235 240

Phe Val Gly Thr Arg Thr
245

<210> 22
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 22
tcctcgatgg agacctgcc 19

<210> 23
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 23
gagaccatgc ccagggagt 19

<210> 24
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 24
tctgggagcc gtcacctt 19

<210> 25
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 25
gacgaggccg aagaggtgg 19

<210> 26

<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 26
gcacaccgga atggatgcg 19

<210> 27
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 27
ccgtcgagct ctgaggtaa 19

<210> 28
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 28
gcccgagccg cacgtgcgt 19

<210> 29
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 29
tgcacgcgt gctgccgacc 20

<210> 30
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 30
ttggcgaagt cgaccaggtc 20

<210> 31
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 31
gccgctcggc acggtgaact tca 23

<210> 32
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 32
atgcgcgtcg tcttctcctc catg 24

<210> 33
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 33
tcatcgtggt tctctccttc c 21

<210> 34
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 34
ggaattcatg accacgaccg atc 23

<210> 35
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 35
cgctccaggt gcaatgccgg gtgcaggc 28

<210> 36
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 36
gatcacgctc ttcgagcggc ag 22

<210> 37
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 37
gaactcgggtg gagtcgatgt c 21

<210> 38
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 38
gttgtcgatc aagacccgca c 21

<210> 39
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 39
catcgtaag gagttcgacg gt 22

<210> 40
<211> 25
<212> DNA
<213> Artificial sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 40
 tgcgcaggctc catgttcacc acgtt 25

 <210> 41
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 41
 gctacgccct ggagagcctg 20

 <210> 42
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 42
 gtcgcggtcg gagagcacga c 21

 <210> 43
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 43
 gccagctcgg cgacgtccat c 21

 <210> 44
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

 <400> 44
 cgacgaggtc gtgcatcag 19

 <210> 45

<211> 56
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 45
aattgatcaa ggtgaacacg gtcatgcgca ggatcctcga gcggaactcc atgggg 56

<210> 46
<211> 56
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 46
ccccatggag ttccgctcga ggatcctgcg catgaccgtg ttcaccttga tcaatt 56

<210> 47
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 47
aactcggtagg agtcgatgtc gtcgctgcgg aa 32

<210> 48
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 48
caatatagga aggatcaaga ggttgac 27

<210> 49
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<220>

<400> 49
tccggagggtg tgctgtcgga cggacttgtc ggtcggaaa 39

<210> 50
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 50
aggagcacta gtgcgggtac tgctgacgtc ctt 33

<210> 51
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 51
gggggatccc atatgcgggt actgctgacg tccttcg 37

<210> 52
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 52
gaaaagatct gccggcgtgg cggcgcgtga gttcctc 37

<210> 53
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 53
agcggcttga tcgtgttgga ccagtac 27

<210> 54
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 54
ggcctatgtg gactacgtgt tgaacgt 27

<210> 55
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 55
aacgcctcgt cctgcagcgg agacacgaac a 31

<210> 56
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 56
ttcgctcccc gatgaacaca actcgta 27

<210> 57
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 57
gaaggagata tacatatgcg cgtcgtcttc tcctc 35

<210> 58
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 58
cgggatcctc atcgtggttc tctccttct gc 32

<210> 59
<211> 32

<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 59
cggtaccat gcgcgtcgtc ttctcctcca tg 32

<210> 60
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 60
cggtacctc atcgtgggtc tctccttcc 29

<210> 61
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 61
Val Thr Gly Ala Gly Asp Gly Asp Ala Asp Val Gln Ala
1 5 10